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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/086,542A

DATE: 08/09/2002  
TIME: 15:49:57

Input Set : N:\Crf3\RULE60\10086542A.RAW  
Output Set: N:\CRF4\08092002\J086542A.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Wahl, Geoffrey M

6 O'Gorman, Stephen V

8 (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN

9 MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL  
10 THEREFOR

12 (iii) NUMBER OF SEQUENCES: 4

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Pretty, Schroeder, Brueggemann &amp; Clark

16 (B) STREET: 444 South Flower Street, Suite 2000

17 (C) CITY: Los Angeles

18 (D) STATE: California

19 (E) COUNTRY: USA

20 (F) ZIP: 90071

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--&gt; 29 (A) APPLICATION NUMBER: US/10/086,542A

C--&gt; 30 (B) FILING DATE: 28-Feb-2002

31 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/484,324

36 (B) FILING DATE: 07-JUN-1995

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Reiter, Stephen E

41 (B) REGISTRATION NUMBER: 31,192

42 (C) REFERENCE/DOCKET NUMBER: P41 9984

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (619) 546-4737

46 (B) TELEFAX: (619) 546-9392

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1380 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: DNA (genomic)

60 (vii) IMMEDIATE SOURCE:

61 (B) CLONE: NATIVE FLP

ENTERED

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/086,542A

DATE: 08/09/2002

TIME: 15:49:58

Input Set : N:\Crf3\RULE60\10086542A.RAW

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63      (ix) FEATURE:
64          (A) NAME/KEY: CDS
65          (B) LOCATION: 1..1269
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT      48
71 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
72   1           5           10           15
74 CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA      96
75 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
76           20           25           30
78 TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC      144
79 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
80           35           40           45
82 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA      192
83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
84   50           55           60
86 AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA      240
87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
88 65           70           75           80
90 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG      288
91 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
92           85           90           95
94 ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT      336
95 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
96           100          105          110
98 CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA      384
99 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
100           115          120          125
102 TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT      432
103 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
104           130          135          140
106 AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA      480
107 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
108 145          150          155          160
110 ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT      528
111 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
112           165          170          175
114 TTA TAC CAA TTC CTC TTC CTA GCT ACT TTC ATC AAT TGT GGA AGA TTC      576
115 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
116           180          185          190
118 AGC GAT ATT AAG AAC GTT GAT CCG AAA TCA TTT AAA TTA GTC CAA AAT      624
119 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
120           195          200          205
122 AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG ACA GAG ACA AAG ACA      672
123 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
124           210          215          220
126 AGC GTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT      720
127 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
128 225          230          235          240

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130	CCA	CTT	GTA	TAT	TTG	GAT	GAA	TTT	TTG	AGG	AAT	TCT	GAA	CCA	GTC	CTA	768
131	Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val	Leu	
132					245				250						255		
134	AAA	CGA	GTA	AAT	AGG	ACC	GGC	AAT	TCT	TCA	AGC	AAT	AAA	CAG	GAA	TAC	816
135	Lys	Arg	Val	Asn	Arg	Thr	Gly	Asn	Ser	Ser	Ser	Asn	Lys	Gln	Glu	Tyr	
136				260				265						270			
138	CAA	TTA	TTA	AAA	GAT	AAC	TTA	GTC	AGA	TCG	TAC	AAT	AAA	GCT	TTG	AAG	864
139	Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys	Ala	Leu	Lys	
140			275					280					285				
142	AAA	AAT	GCG	CCT	TAT	TCA	ATC	TTT	GCT	ATA	AAA	AAT	GGC	CCA	AAA	TCT	912
143	Lys	Asn	Ala	Pro	Tyr	Ser	Ile	Phe	Ala	Ile	Lys	Asn	Gly	Pro	Lys	Ser	
144		290					295				300						
146	CAC	ATT	GGA	AGA	CAT	TTG	ATG	ACC	TCA	TTT	CTT	TCA	ATG	AAG	GGC	CTA	960
147	His	Ile	Gly	Arg	His	Leu	Met	Thr	Ser	Phe	Leu	Ser	Met	Lys	Gly	Leu	
148	305				310					315					320		
150	ACG	GAG	TTG	ACT	AAT	GTT	GTG	GGA	AAT	TGG	AGC	GAT	AAG	CGT	GCT	TCT	1008
151	Thr	Glu	Leu	Thr	Asn	Val	Val	Gly	Asn	Trp	Ser	Asp	Lys	Arg	Ala	Ser	
152				325					330					335			
154	GCC	GTG	GCC	AGG	ACA	ACG	TAT	ACT	CAT	CAG	ATA	ACA	GCA	ATA	CCT	GAT	1056
155	Ala	Val	Ala	Arg	Thr	Thr	Tyr	Thr	His	Gln	Ile	Thr	Ala	Ile	Pro	Asp	
156			340					345					350				
158	CAC	TAC	TTC	GCA	CTA	GTT	TCT	CGG	TAC	TAT	GCA	TAT	GAT	CCA	ATA	TCA	1104
159	His	Tyr	Phe	Ala	Leu	Val	Ser	Arg	Tyr	Tyr	Ala	Tyr	Asp	Pro	Ile	Ser	
160		355					360				365						
162	AAG	GAA	ATG	ATA	GCA	TTG	AAG	GAT	GAG	ACT	AAT	CCA	ATT	GAG	GAG	TGG	1152
163	Lys	Glu	Met	Ile	Ala	Leu	Lys	Asp	Glu	Thr	Asn	Pro	Ile	Glu	Glu	Trp	
164		370				375					380						
166	CAG	CAT	ATA	GAA	CAG	CTA	AAG	GGT	AGT	GCT	GAA	GGA	AGC	ATA	CGA	TAC	1200
167	Gln	His	Ile	Glu	Gln	Leu	Lys	Gly	Ser	Ala	Glu	Gly	Ser	Ile	Arg	Tyr	
168	385				390				395					400			
170	CCC	GCA	TGG	ATT	GGG	ATA	ATA	TCA	CAG	GAG	GTA	CTA	GAC	TAC	CTT	TCA	1248
171	Pro	Ala	Trp	Ile	Gly	Ile	Ile	Ser	Gln	Glu	Val	Leu	Asp	Tyr	Leu	Ser	
172			405					410					415				
174	TCC	TAC	ATA	AAT	AGA	CGC	ATA	TAAGTACGCA	TTTAAGCATA	AACACGCACT							1299
175	Ser	Tyr	Ile	Asn	Arg	Arg	Ile										
176			420														
178	ATCCCGTTCT	TCTCATGTAT	ATATATATAC	AGGCAACACG	CAGATATAGG	TGCCACGTGA											1359
180	ACAGTGAGCT	GTATGTGCGC	A														1380
183	(2) INFORMATION FOR SEQ ID NO: 2:																
185	(i) SEQUENCE CHARACTERISTICS:																
186	(A) LENGTH: 423 amino acids																
187	(B) TYPE: amino acid																
188	(D) TOPOLOGY: linear																
190	(ii) MOLECULE TYPE: protein																
192	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:																
194	Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu	Val	
195	1				5				10					15			
197	Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys	Ile	Ala	
198			20				25					30					

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200 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
201          35                      40                      45
203 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
204          50                      55                      60
206 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
207 65                      70                      75                      80
209 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
210                      85                      90                      95
212 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
213          100                      105                      110
215 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
216          115                      120                      125
218 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
219          130                      135                      140
221 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
222 145                      150                      155                      160
224 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
225          165                      170                      175
227 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
228          180                      185                      190
230 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
231          195                      200                      205
233 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
234          210                      215                      220
236 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
237 225                      230                      235                      240
239 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
240          245                      250                      255
242 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
243          260                      265                      270
245 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
246          275                      280                      285
248 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
249          290                      295                      300
251 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
252 305                      310                      315                      320
254 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
255          325                      330                      335
257 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
258          340                      345                      350
260 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
261          355                      360                      365
263 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
264          370                      375                      380
266 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
267 385                      390                      395                      400
269 Pro Ala Trp Ile Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
270          405                      410                      415
272 Ser Tyr Ile Asn Arg Arg Ile

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273 420

275 (2) INFORMATION FOR SEQ ID NO: 3:

277 (i) SEQUENCE CHARACTERISTICS:

278 (A) LENGTH: 34 base pairs

279 (B) TYPE: nucleic acid

280 (C) STRANDEDNESS: single

281 (D) TOPOLOGY: linear

283 (ii) MOLECULE TYPE: DNA (genomic)

287 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

289 GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC 34

291 (2) INFORMATION FOR SEQ ID NO: 4:

293 (i) SEQUENCE CHARACTERISTICS:

294 (A) LENGTH: 68 base pairs

295 (B) TYPE: nucleic acid

296 (C) STRANDEDNESS: single

297 (D) TOPOLOGY: linear

299 (ii) MOLECULE TYPE: DNA (genomic)

303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

305 GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG 60

307 GAACTTCA 68

## VERIFICATION SUMMARY

DATE: 08/09/2002

PATENT APPLICATION: US/10/086,542A

TIME: 15:49:59

Input Set : N:\Crf3\RULE60\10086542A.RAW

Output Set: N:\CRF4\08092002\J086542A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]